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TECH CENTER 1600/29

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 3 <110> APPLICANT: NAMPOOTHIRI, Madhavan et al.
 5 <120> TITLE OF INVENTION: Nucleotide Sequences Which Code for the fadD15 Gene
 7 <130> FILE REFERENCE: 032301 WN 1181
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/855,750A
C--> 9 <141> CURRENT FILING DATE: 2002-12-17
 9 <160> NUMBER OF SEQ ID NOS: 4
11 <170> SOFTWARE: PatentIn version 3.1
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 2300
15 <212> TYPE: DNA
16 <213> ORGANISM: Corynebacterium glutamicum
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41 aaatacatct tttggattgg gctttggggt ggctttttata caccctgatt ggtgcagata     120
43 taagaagtta ttgacacact gaatacatag agaaaaattc catgtggtta aagatatgcc     180
45 taaagatctg accaaaaacg tgactaaaga cgtgacgaca caagtacagc caaattaaag     240
47 gaaagg ttg aat ttg acc atg act tca cct aat acc ctg cag gaa tac        288
48        Met Asn Leu Thr Met Thr Ser Pro Asn Thr Leu Gln Glu Tyr
49         1               5                   10
51 act gaa cct gcc aag tac acc atc gga gaa tct gaa acc tgc ctg acc       336
52 Thr Glu Pro Ala Lys Tyr Thr Ile Gly Glu Ser Glu Thr Cys Leu Thr
53 15              20                  25                  30
55 gcc ctt cta gat cag att aag act cga cct tac gga gtt ttg ttc agc      384
56 Ala Leu Leu Asp Gln Ile Lys Thr Arg Pro Tyr Gly Val Leu Phe Ser
57              35                  40                  45
59 aag cct gcc aac tat gag tgg gtg aat gta act gcc aaa gaa ttt cag      432
60 Lys Pro Ala Asn Tyr Glu Trp Val Asn Val Thr Ala Lys Glu Phe Gln
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DJS

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61            50              55              60
63 gac gag gtt ttt gcg gtt gca aaa gga att att tca gtc ggc gta gag    480
64 Asp Glu Val Phe Ala Val Ala Lys Gly Ile Ile Ser Val Gly Val Glu
65         65              70              75
67 cag gga gac cgt gtc gcg ctg ctg tcc aat act cgc tat gag tgg gct    528
68 Gln Gly Asp Arg Val Ala Leu Leu Ser Asn Thr Arg Tyr Glu Trp Ala
69      80              85              90
71 gtg ctt gat ttc gct atc tgg gcc gct ggc gca gtg agc gtg cct atc    576
72 Val Leu Asp Phe Ala Ile Trp Ala Ala Gly Ala Val Ser Val Pro Ile
73 95             100             105             110
75 tac agc tcc tct tca ctg tcc caa att gag tgg atc att gag gat tcc    624
76 Tyr Ser Ser Ser Ser Leu Ser Gln Ile Glu Trp Ile Ile Glu Asp Ser
77             115             120             125
79 ggc gct gtt ttg gcc att acc gaa acc cct gat cat acc gac ttg atg    672
80 Gly Ala Val Leu Ala Ile Thr Glu Thr Pro Asp His Thr Asp Leu Met
81             130             135             140
83 aag aac ctg gtc atc ggt gaa gac gga act cca gcg att aag ggt tca    720
84 Lys Asn Leu Val Ile Gly Glu Asp Gly Thr Pro Ala Ile Lys Gly Ser
85         145             150             155
87 cct tcc aag ctg cgc cgc att cta gag atc aac tct tcg gcg ttg gag    768
88 Pro Ser Lys Leu Arg Arg Ile Leu Glu Ile Asn Ser Ser Ala Leu Glu
89      160             165             170
91 acc ttg aag ttt gag ggc cgc gag ctt tct gat gag ctg gtg tgg gaa    816
92 Thr Leu Lys Phe Glu Gly Arg Glu Leu Ser Asp Glu Leu Val Trp Glu
93 175             180             185             190
95 cgc att cat gca acc aag gcc gct gac ctg gcg tct ttg gtg tac acc    864
96 Arg Ile His Ala Thr Lys Ala Ala Asp Leu Ala Ser Leu Val Tyr Thr
97             195             200             205
99 tct ggc aca act ggt agg ccg aag ggc tgc gag ttg tcc cac tac cac    912
100 Ser Gly Thr Thr Gly Arg Pro Lys Gly Cys Glu Leu Ser His Tyr His
101             210             215             220
103 tgg ttg gct gag gtc cga gcg ctg atc acc aat gac atc gga gcg atc    960
104 Trp Leu Ala Glu Val Arg Ala Leu Ile Thr Asn Asp Ile Gly Ala Ile
105         225             230             235
107 gcg atg cca ggt tca agg ttg ctc acc ttc ctt cct ttg gcg cac gtt   1008
108 Ala Met Pro Gly Ser Arg Leu Leu Thr Phe Leu Pro Leu Ala His Val
109      240             245             250
111 ctt gct cgc gca gtg cac ttg gcc ttc gct gtc acc ggt gca acc cag   1056
112 Leu Ala Arg Ala Val His Leu Ala Phe Ala Val Thr Gly Ala Thr Gln
113 255             260             265             270
115 tcc cac tgg tct gat ttc agc acc ctt act ttg gaa ctg cag cgt tcc   1104
116 Ser His Trp Ser Asp Phe Ser Thr Leu Thr Leu Glu Leu Gln Arg Ser
117             275             280             285
119 cgc ccg aac ctg att ttg ggt gtt cca cgc gtg ttt gaa aag gtc cgc   1152
120 Arg Pro Asn Leu Ile Leu Gly Val Pro Arg Val Phe Glu Lys Val Arg
121             290             295             300
123 aac gcc gct gct gct aat gct gct gac ggt ggc gca atc aag cgc atc   1200
124 Asn Ala Ala Ala Ala Asn Ala Ala Asp Gly Gly Ala Ile Lys Arg Ile
125         305             310             315
```

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127  atg ttt gag cgt gcc gaa aag gcg gcc att gaa tac tcc atg gct ctt       1248
128  Met Phe Glu Arg Ala Glu Lys Ala Ala Ile Glu Tyr Ser Met Ala Leu
129      320                 325                 330
131  gat act gca gaa ggc cca agc aag tcc cag gtt atg gca cat aaa gcg       1296
132  Asp Thr Ala Glu Gly Pro Ser Lys Ser Gln Val Met Ala His Lys Ala
133  335                 340                 345                 350
135  ttt gac aag ctg gtg tac tcc aag atc cgt gca gct gtc ggt ggc gat       1344
136  Phe Asp Lys Leu Val Tyr Ser Lys Ile Arg Ala Ala Val Gly Gly Asp
137                  355                 360                 365
139  gtg cag tac gcc atc acc ggt ggt tca gcg atg ggg cag gag ctg ctg       1392
140  Val Gln Tyr Ala Ile Thr Gly Gly Ser Ala Met Gly Gln Glu Leu Leu
141                  370                 375                 380
143  cac ttc ttc cgc ggt gtg ggc atg acc atc tac gaa ggt tat ggt ctg       1440
144  His Phe Phe Arg Gly Val Gly Met Thr Ile Tyr Glu Gly Tyr Gly Leu
145          385                 390                 395
147  acg gaa tct gcg gct gct gca gcg gtg gac ttc act gat caa aag atc       1488
148  Thr Glu Ser Ala Ala Ala Ala Ala Val Asp Phe Thr Asp Gln Lys Ile
149      400                 405                 410
151  ggc act gtg ggt aag ccg atg ggt ggc atg acc atc aag atc aat gaa       1536
152  Gly Thr Val Gly Lys Pro Met Gly Gly Met Thr Ile Lys Ile Asn Glu
153  415                 420                 425                 430
155  gat ggc gaa atc atg cta aaa ggc gag atg ttg ttc cag gga tat tgg       1584
156  Asp Gly Glu Ile Met Leu Lys Gly Glu Met Leu Phe Gln Gly Tyr Trp
157                  435                 440                 445
159  aac aac cca gaa gcc aca gca gaa gcc ctc cac gac ggt tgg ttc aac       1632
160  Asn Asn Pro Glu Ala Thr Ala Glu Ala Leu His Asp Gly Trp Phe Asn
161          450                 455                 460
163  acc ggc gat ctg ggt gag ctg ttg gag tct gga cac ctg gtg atc acc       1680
164  Thr Gly Asp Leu Gly Glu Leu Leu Glu Ser Gly His Leu Val Ile Thr
165          465                 470                 475
167  gga cgt aag aaa gat ctg atc gtg acc gcg ggc ggc aag aac gtt tcc       1728
168  Gly Arg Lys Lys Asp Leu Ile Val Thr Ala Gly Gly Lys Asn Val Ser
169      480                 485                 490
171  cca gga ccc atg gaa gac atc atc cgc gca cac cca ctg gtc agc cag       1776
172  Pro Gly Pro Met Glu Asp Ile Ile Arg Ala His Pro Leu Val Ser Gln
173  495                 500                 505                 510
175  gcc atg gtg gtg ggc gat ggt aaa cca ttc gtt ggc ctg ctg gtg acc       1824
176  Ala Met Val Val Gly Asp Gly Lys Pro Phe Val Gly Leu Leu Val Thr
177                  515                 520                 525
179  ttg gat cca gat atg ttg aag cgg tgg aag ctg aac cac aac att gcg       1872
180  Leu Asp Pro Asp Met Leu Lys Arg Trp Lys Leu Asn His Asn Ile Ala
181                  530                 535                 540
183  gaa tcc cgc acg gtt tct gag att gct act gat cct gca ctg cgt gcg       1920
184  Glu Ser Arg Thr Val Ser Glu Ile Ala Thr Asp Pro Ala Leu Arg Ala
185          545                 550                 555
187  gaa atc cag gat gca gtc aac aac gct aat gcc acg gtg tct cat tca       1968
188  Glu Ile Gln Asp Ala Val Asn Asn Ala Asn Ala Thr Val Ser His Ser
189      560                 565                 570
191  gag gcg atc aag cgg ttc tac atc ctt gat cgc gac ctg acc gag gaa       2016
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RAW SEQUENCE LISTING   DATE: 01/07/2003
PATENT APPLICATION: **US/09/855,750A**   TIME: 14:05:58

Input Set : **A:\032301.1181.ST25.txt**
Output Set: **N:\CRF4\01072003\I855750A.raw**

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192 Glu Ala Ile Lys Arg Phe Tyr Ile Leu Asp Arg Asp Leu Thr Glu Glu
193 575.                  580              585              590
195 gcc gac gag ctg acc cca acg ctg aag gtc aag cgc aac gtt gtt gtt        2064
196 Ala Asp Glu Leu Thr Pro Thr Leu Lys Val Lys Arg Asn Val Val Val
197                  595              600              605
199 cgc cgt tac gca gac gcc atc gac cac atc tac aac cga tgagtaacac         2113
200 Arg Arg Tyr Ala Asp Ala Ile Asp His Ile Tyr Asn Arg
201                  610              615
203 agagaccaa tttgattggg atggatcgac atggacccgc accgaagtcg gcgaagcacc       2173
205 aacacgcttc gctgtgggcg tgatggagga tttcgcctac attgcagcca ctggcacgga      2233
207 cgggggatgaa gagttcttta ctttgggctc aaatccgggt ctgacgtttg gtgatcccga     2293
209 gtggctt                                                                2300
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213 <211> LENGTH: 619
214 <212> TYPE: PRT
215 <213> ORGANISM: Corynebacterium glutamicum
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219 Met Asn Leu Thr Met Thr Ser Pro Asn Thr Leu Gln Glu Tyr Thr Glu
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224                  20               25                30
227 Leu Asp Gln Ile Lys Thr Arg Pro Tyr Gly Val Leu Phe Ser Lys Pro
228               35               40                45
231 Ala Asn Tyr Glu Trp Val Asn Val Thr Ala Lys Glu Phe Gln Asp Glu
232        50               55               60
235 Val Phe Ala Val Ala Lys Gly Ile Ile Ser Val Gly Val Glu Gln Gly
236 65                 70               75                80
239 Asp Arg Val Ala Leu Leu Ser Asn Thr Arg Tyr Glu Trp Ala Val Leu
240               85 ·              90                95
243 Asp Phe Ala Ile Trp Ala Ala Gly Ala Val Ser Val Pro Ile Tyr Ser
244               100              105              110
247 Ser Ser Ser Leu Ser Gln Ile Glu Trp Ile Ile Glu Asp Ser Gly Ala
248               115              120              125
251 Val Leu Ala Ile Thr Glu Thr Pro Asp His Thr Asp Leu Met Lys Asn
252        130              135              140
255 Leu Val Ile Gly Glu Asp Gly Thr Pro Ala Ile Lys Gly Ser Pro Ser
256 145              150              155              160
259 Lys Leu Arg Arg Ile Leu Glu Ile Asn Ser Ser Ala Leu Glu Thr Leu
260               165              170              175
263 Lys Phe Glu Gly Arg Glu Leu Ser Asp Glu Leu Val Trp Glu Arg Ile
264               180              185              190
267 His Ala Thr Lys Ala Ala Asp Leu Ala Ser Leu Val Tyr Thr Ser Gly
268        195              200              205
271 Thr Thr Gly Arg Pro Lys Gly Cys Glu Leu Ser His Tyr His Trp Leu
272        210              215              220
275 Ala Glu Val Arg Ala Leu Ile Thr Asn Asp Ile Gly Ala Ile Ala Met
276 225              230              235              240
279 Pro Gly Ser Arg Leu Leu Thr Phe Leu Pro Leu Ala His Val Leu Ala
280               245              250              255
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283 Arg Ala Val His Leu Ala Phe Ala Val Thr Gly Ala Thr Gln Ser His
284         260             265             270
287 Trp Ser Asp Phe Ser Thr Leu Thr Leu Glu Leu Gln Arg Ser Arg Pro
288         275             280             285
291 Asn Leu Ile Leu Gly Val Pro Arg Val Phe Glu Lys Val Arg Asn Ala
292     290             295             300
295 Ala Ala Ala Asn Ala Ala Asp Gly Gly Ala Ile Lys Arg Ile Met Phe
296 305             310 .             315                 320
299 Glu Arg Ala Glu Lys Ala Ala Ile Glu Tyr Ser Met Ala Leu Asp Thr
300             325             330             335
303 Ala Glu Gly Pro Ser Lys Ser Gln Val Met Ala His Lys Ala Phe Asp
304             340             345             350
307 Lys Leu Val Tyr Ser Lys Ile Arg Ala Ala Val Gly Gly Asp Val Gln
308         355             360             365
311 Tyr Ala Ile Thr Gly Gly Ser Ala Met Gly Gln Glu Leu Leu His Phe
312     370             375             380
315 Phe Arg Gly Val Gly Met Thr Ile Tyr Glu Gly Tyr Gly Leu Thr Glu
316 385             390             395                 400
319 Ser Ala Ala Ala Ala Ala Val Asp Phe Thr Asp Gln Lys Ile Gly Thr
320             405             410             415
323 Val Gly Lys Pro Met Gly Gly Met Thr Ile Lys Ile Asn Glu Asp Gly
324             420             425             430.
327 Glu Ile Met Leu Lys Gly Glu Met Leu Phe Gln Gly Tyr Trp Asn Asn
328         435             440             445
331 Pro Glu Ala Thr Ala Glu Ala Leu His Asp Gly Trp Phe Asn Thr Gly
332     450             455             460
335 Asp Leu Gly Glu Leu Leu Glu Ser Gly His Leu Val Ile Thr Gly Arg
336 465             470             475                 480
339 Lys Lys Asp Leu Ile Val Thr Ala Gly Gly Lys Asn Val Ser Pro Gly
340             485             490             495
343 Pro Met Glu Asp Ile Ile Arg Ala His Pro Leu Val Ser Gln Ala Met
344         500             505             510
347 Val Val Gly Asp Gly Lys Pro Phe Val Gly Leu Leu Val Thr Leu Asp
348     515             520             525
351 Pro Asp Met Leu Lys Arg Trp Lys Leu Asn His Asn Ile Ala Glu Ser
352     530             535 .             540
355 Arg Thr Val Ser Glu Ile Ala Thr Asp Pro Ala Leu Arg Ala Glu Ile
356 545             550             555                 560
359 Gln Asp Ala Val Asn Asn Ala Asn Ala Thr Val Ser His Ser Glu Ala
360             565             570             575
363 Ile Lys Arg Phe Tyr Ile Leu Asp Arg Asp Leu Thr Glu Glu Ala Asp
364         580             585             590
367 Glu Leu Thr Pro Thr Leu Lys Val Lys Arg Asn Val Val Val Arg Arg
368     595             600             605
371 Tyr Ala Asp Ala Ile Asp His Ile Tyr Asn Arg
372     610             615
375 <210> SEQ ID NO: 3
376 <211> LENGTH: 24
377 <212> TYPE: DNA
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/855,750A**

DATE: 01/07/2003
TIME: 14:06:00

Input Set : **A:\032301.1181.ST25.txt**
Output Set: **N:\CRF4\01072003\I855750A.raw**

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L:9  M:270 C: Current Application Number differs, Replaced Current Application No
L:9  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:28 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:21
L:33 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:26
L:38 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:31
L:38 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:36
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